WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising the amino acid sequences selected from the group consisting of SEQ ID NOS: 2 and 4, and fragments thereof.

2. The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 79 to 88 of SEQ ID NO: 2.

3. The isolated polypeptide of Claim 1, wherein the fragments comprise the amino acid residues 236 to 245 of SEQ ID NO: 4.

4. An isolated nucleic acid comprising the nucleotide sequence selected from the group consisting of SEQ ID NOS: 1 and 3, and fragments thereof.

5. The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 314 to 319 of SEQ ID NO: 1.

6. The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 304 to 333 of SEQ ID NO: 1.

7. The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 790 to 795 of SEQ ID NO: 3.

8. The isolated nucleic acid of Claim 4, wherein the fragments comprise nucleotides 775 to 804 of SEQ ID NO: 3.

9. An expression vector comprising the nucleic acid of Claim 4.

10. A host cell transformed with the expression vector of Claim 9.

11. A method for producing the polypeptide of Claim 1, which comprises the steps of:

(1) culturing the host cell of Claim 10 under a condition suitable for the expression of the polypeptide; and

(2) recovering the polypeptide from the host cell culture.

12. An antibody specifically binding to the polypeptide of Claim 1.

13. A method for diagnosing the diseases associated with the deficiency of the ARL gene in a mammal, in particular cancers, which comprises detecting the nucleic acid of Claim 4 or the polypeptide of Claim 1.

14. The method of Claim 13, wherein the detection of the nucleic acid of Claim 4 comprises the steps of:

(1) extracting total RNA from a sample obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;

(3) bringing the cDNA sample into contact with the nucleic acid of Claim 4; and

(4) detecting whether the cDNA hybridizes with the nucleic acid of Claim 4.

15. The method of Claim 14 further comprising the step of determining the amount of hybridized sample.

16. The method of Claim 13, wherein the detection of the nucleic acid of Claim 4 comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA

comprising the fragments comprising nucleotide 314 to 319 of SEQ ID NO: 1 or nucleotide 790 to 795 of SEQ ID NO: 3; and

(3) detecting whether the cDNA is obtained.

17. The method of Claim 13, wherein the detection of the nucleic acid of Claim 4 comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotide 304 to 333 of SEQ ID NO: 1 or nucleotide 775 to 804 of SEQ ID NO: 3; and

(3) detecting whether the cDNA is obtained.

18. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 314 to 319 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 319, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 314 to 319 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 314.

19. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 304 to 333 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 333, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 304 to 333 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 304.

20. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 790 to 795 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 795, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 790 to 795 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 790.

21. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 775 to 804 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 804, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 775 to 804 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 775.

22. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 314 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 319.

23. The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 790 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 795.

24. The method of Claim 22, the cDNA sample amplified from SEQ ID NO: 1 is 247bp shorter than that from ARL.

25. The method of Claim 23, the cDNA sample amplified from SEQ ID NO: 3 is 58bp shorter than that from ARL.

26. The method of Claim 16 further comprising the step of detecting the amount of the amplified cDNA sample.

27. The method of Claim 13, wherein the detection of the polypeptide of Claim 1 comprises the steps of contacting the antibody of Claim 12 with protein samples extracted from the mammal, and detecting whether an antibody-polypeptide complex is formed.

28. The method of Claim 27 further comprising the step of determining the amount of the antibody-polypeptide complex.